


In the Application of:		Docket No.:	3198
Jonathan M.J. Derry, William C. Fanslow, III, and William C. Dougall		Group Art Unit:	Unknown
Serial No:	--to be assigned--	Examiner:	Unknown
Filed:	May 8, 2001		
For:	SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING		

BOX PATENT APPLICATION  
Assistant Commissioner for Patents  
Washington, D.C. 20231

Applicants by their undersigned representative hereby state that the contents of the paper copy and the computer-readable copy of the Sequence Listing submitted herewith are the same.

  
Patricia Anne Perkins  
Registration No. 34,693

Immunex Corporation  
Law Department  
51 University Street  
Seattle, WA 98101  
Telephone (206) 587-0430

## SEQUENCE LISTING

<110> Derry, Jonathan  
Fanslow, William  
Dougall, William

<120> SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING

<130> 3198

<140> --to be assigned--

<141> 2001-05-08

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 1994

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (149)..(1405)

<400> 1

```

ggcacgagca tggcccttgt gatccaggtg gggaaactaa ggcccagaga agtgaggacc      60
ccgcagacta tcaatcccag tctcttcccc tcactccctg tgaagctctc cagcatcatc      120
gaggtcccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc      172
                               Met Asn Arg His Leu Trp Lys Ser
                               1                               5

caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag      220
Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln
   10                               15                               20

gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac      268
Asp Val Leu Gly Glu Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His
   25                               30                               35                               40

ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag      316
Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu
           45                               50                               55

gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg      364
Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu
           60                               65                               70

cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag      412
Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu
           75                               80                               85

gag aag gag ttc ctc atg tgc aag ttc cag gag gcc agg aaa ctg gtg      460
Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val
           90                               95                               100

```

095167-05001

gag Glu 105	aga Arg	ctc Leu	ggc Gly	ctg Leu	gag Glu 110	aag Lys	ctc Leu	gat Asp	ctg Leu	aag Lys 115	agg Arg	cag Gln	aag Lys	gag Glu 120	cag Gln	508
gct Ala	ctg Leu	cgg Arg	gag Glu	gtg Val 125	gag Glu	cac His	ctg Leu	aag Lys	aga Arg 130	tgc Cys	cag Gln	cag Gln	cag Gln	atg Met 135	gct Ala	556
gag Glu	gac Asp	aag Lys	gcc Ala 140	tct Ser	gtg Val	aaa Lys	gcc Ala	cag Gln 145	gtg Val	acg Thr	tcc Ser	ttg Leu	ctc Leu 150	ggg Gly	gag Glu	604
ctg Leu	cag Gln 155	gag Glu	agc Ser	cag Gln	agt Ser	cgc Arg	ttg Leu 160	gag Glu	gct Ala	gcc Ala	act Thr 165	aag Lys	gaa Glu	tgc Cys	cag Gln	652
gct Ala 170	ctg Leu	gag Glu	ggt Gly	cgg Arg	gcc Ala	cgg Arg 175	gcg Ala	gcc Ala	agc Ser	gag Glu 180	cag Gln	gcg Ala	cgg Arg	cag Gln	ctg Leu	700
gag Glu 185	agt Ser	gag Glu	cgc Arg	gag Glu	gcg Ala	ctg Leu	cag Gln	cag Gln	cag Gln	cac His 195	agc Ser	gtg Val	cag Gln	gtg Val	gac Asp 200	748
cag Gln	ctg Leu	cgc Arg	atg Met 205	cag Gln	ggc Gly	cag Gln	agc Ser	gtg Val 210	gag Glu	gcc Ala	gcg Ala	ctc Leu	cgc Arg	atg Met 215	gag Glu	796
cgc Arg	cag Gln	gcc Ala	gcc Ala 220	tcg Ser	gag Glu	gag Glu	aag Lys	agg Arg 225	aag Lys	ctg Leu	gcc Ala	cag Gln	ttg Leu 230	cag Gln	gtg Val	844
gcc Ala	tat Tyr	cac His 235	cag Gln	ctc Leu	ttc Phe	caa Gln	gaa Glu 240	tac Tyr	gac Asp	aac Asn	cac His	atc Ile 245	aag Lys	agc Ser	agc Ser	892
gtg Val 250	gtg Val	ggc Gly	agt Ser	gag Glu	cgg Arg	aag Lys 255	cga Arg	gga Gly	atg Met	cag Gln 260	ctg Leu	gaa Glu	gat Asp	ctc Leu	aaa Lys	940
cag Gln 265	cag Gln	ctc Leu	cag Gln	cag Gln 270	gcc Ala	gag Glu	gag Glu	gcc Ala	ctg Leu 275	gtg Val	gcc Ala	aaa Lys	cag Gln	gag Glu 280	gtg Val	988
atc Ile	gat Asp	aag Lys	ctg Leu	aag Lys 285	gag Glu	gag Glu	gcc Ala	gag Glu 290	cag Gln	cac His	aag Lys	att Ile	gtg Val	atg Met 295	gag Glu	1036
acc Thr	gtt Val	ccg Pro	gtg Val 300	ctg Leu	aag Lys	gcc Ala	cag Gln	gcg Ala 305	gat Asp	atc Ile	tac Tyr	aag Lys	gcg Ala	gac Asp 310	ttc Phe	1084
cag Gln	gct Ala	gag Glu 315	agg Arg	cag Gln	gcc Ala	cgg Arg	gag Glu 320	aag Lys	ctg Leu	gcc Ala	gag Glu 325	aag Lys	aag Lys	gag Glu	ctc Leu	1132
ctg Leu	cag Gln 330	gag Glu	cag Gln	ctg Leu	gag Glu	cag Gln 335	ctg Leu	cag Gln	agg Arg	gag Glu 340	tac Tyr	agc Ser	aaa Lys	ctg Leu	aag Lys	1180

```

gcc agc tgt cag gag tcg gcc agg atc gag gac atg agg aag cgg cat      1228
Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu Asp Met Arg Lys Arg His
345                      350                      355                      360

gtc gag gtc tcc cag gcc ccc ttg ccc ccc gcc cct gcc tac ctc tcc      1276
Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr Leu Ser
                      365                      370                      375

tct ccc ctg gcc ctg ccc agc cag agg agg agc ccc ccc gag gag cca      1324
Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg Ser Pro Pro Glu Glu Pro
                      380                      385                      390

cct gac ttc tgc tgt ccc aag tgc cag tat cag gcc cct gat atg gac      1372
Pro Asp Phe Cys Cys Pro Lys Cys Gln Tyr Gln Ala Pro Asp Met Asp
                      395                      400                      405

acc ctg cag ata cat gtc atg gag tgc att gag tagggccggc cagtgaagg      1425
Thr Leu Gln Ile His Val Met Glu Cys Ile Glu
410                      415

ccactgctg cccgaggacg tgcccgggac cgtgcagtct gcgctttcct ctcccgctg      1485

cctagcccag gatgaagggc tgggtggcca caactgggat gccacctgga gcccaccca      1545

ggagctggcc gcggcacctt acgcttcagc tgttgatccg ctggtcccct cttttggggt      1605

agatgcggcc ccgatcaggc ctgactcgct gctctttttg ttcccttctg tctgctcgaa      1665

ccacttgccct cgggctaata cctccctctt cctccacccg gcactgggga agtcaagaat      1725

ggggcctggg gctctcaggg agaactgctt cccctggcag agctgggtgg cagctcttcc      1785

tcccaccgga caccgacccg ccgcgcgctg tgccctggga gtgctgccct cttaccatgc      1845

acacgggtgc tctccttttg ggctgcatgc tattccattt tgcagccaga ccgatgtgta      1905

ttaaaccagt cactattgat ggacatttgg gttgtttccc atctttttgt taccataaat      1965

aatggcatag taaaaaaaaa aaaaaaaaaa      1994

```

<210> 2  
 <211> 419  
 <212> PRT  
 <213> Homo sapiens

<400> 2

```

Met Asn Arg His Leu Trp Lys Ser Gln Leu Cys Glu Met Val Gln Pro
1                      5                      10                      15

```

```

Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Glu Ser Pro
20                      25                      30

```

```

Leu Gly Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro
35                      40                      45

```

Glu Thr Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala  
50 55 60

Ile Arg Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu  
65 70 75 80

His Phe Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys  
85 90 95

Phe Gln Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu  
100 105 110

Asp Leu Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu  
115 120 125

Lys Arg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala  
130 135 140

Gln Val Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu  
145 150 155 160

Glu Ala Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala  
165 170 175

Ala Ser Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln  
180 185 190

Gln Gln His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Ser  
195 200 205

Val Glu Ala Ala Leu Arg Met Glu Arg Gln Ala Ala Ser Glu Glu Lys  
210 215 220

Arg Lys Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu  
225 230 235 240

Tyr Asp Asn His Ile Lys Ser Ser Val Val Gly Ser Glu Arg Lys Arg  
245 250 255

Gly Met Gln Leu Glu Asp Leu Lys Gln Gln Leu Gln Gln Ala Glu Glu  
260 265 270

Ala Leu Val Ala Lys Gln Glu Val Ile Asp Lys Leu Lys Glu Glu Ala  
275 280 285

Glu Gln His Lys Ile Val Met Glu Thr Val Pro Val Leu Lys Ala Gln  
290 295 300

Ala Asp Ile Tyr Lys Ala Asp Phe Gln Ala Glu Arg Gln Ala Arg Glu  
305 310 315 320

Lys Leu Ala Glu Lys Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu  
325 330 335

Gln Arg Glu Tyr Ser Lys Leu Lys Ala Ser Cys Gln Glu Ser Ala Arg  
340 345 350

Ile Glu Asp Met Arg Lys Arg His Val Glu Val Ser Gln Ala Pro Leu  
355 360 365

Pro Pro Ala Pro Ala Tyr Leu Ser Ser Pro Leu Ala Leu Pro Ser Gln  
370 375 380

Arg Arg Ser Pro Pro Glu Glu Pro Pro Asp Phe Cys Cys Pro Lys Cys  
385 390 395 400

Gln Tyr Gln Ala Pro Asp Met Asp Thr Leu Gln Ile His Val Met Glu  
405 410 415

Cys Ile Glu

<210> 3  
<211> 5371  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (392)..(3262)

<400> 3  
gggggcgggc ccaggtagca ggtttggctg cgcggggggc gcgcgtcgga gtttccccct 60  
ttctaggggtg aggatgggtc tacacagcca cccggagttc cttagttgaa aggtgcgccc 120  
tgctgtgaca gaatgtggtg attgtaatct ttaacatttt catgtaaaac atatttcctg 180  
atcatctttc cattgtcttc atggaaaatt gataaatatt tgtgccttcc aactctcgtc 240  
ttgggtgaat gacttcatct taatacaaca tggacaccac gttgctgaaa acatgctttg 300  
ggactgccac tgaatttatc ttttgcggtt ttatgacaaa gttattagta gtttcccttt 360  
tttgaattag tattttgaag ttaatatcac a atg agt tca ggc tta tgg agc 412  
Met Ser Ser Gly Leu Trp Ser  
1 5



aca gtt ata ttc tgt gat gtt ttg cca gga aaa gaa agc tta gga tat	1180
Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys Glu Ser Leu Gly Tyr	
250 255 260	
ttt gtt ggt gtg gac atg gat aac cct att ggc aac tgg gat gga aga	1228
Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly Asn Trp Asp Gly Arg	
265 270 275	
ttt gat gga gtg cag ctt tgt agt ttt gcg tgt gtt gaa agt aca att	1276
Phe Asp Gly Val Gln Leu Cys Ser Phe Ala Cys Val Glu Ser Thr Ile	
280 285 290 295	
cta ttg cac atc aat gat atc atc cca gct tta tca gag agt gtg acg	1324
Leu Leu His Ile Asn Asp Ile Ile Pro Ala Leu Ser Glu Ser Val Thr	
300 305 310	
cag gaa agg agg cct ccc aaa ctt gcc ttt atg tca aga ggt gtt ggg	1372
Gln Glu Arg Arg Pro Pro Lys Leu Ala Phe Met Ser Arg Gly Val Gly	
315 320 325	
gac aaa ggt tca tcc agt cat aat aaa cca aag gct aca gga tct acc	1420
Asp Lys Gly Ser Ser Ser His Asn Lys Pro Lys Ala Thr Gly Ser Thr	
330 335 340	
tca gac cct gga aat aga aac aga tct gaa tta ttt tat acc tta aat	1468
Ser Asp Pro Gly Asn Arg Asn Arg Ser Glu Leu Phe Tyr Thr Leu Asn	
345 350 355	
ggg tct tct gtt gac tca caa cca caa tcc aaa tca aaa aat aca tgg	1516
Gly Ser Ser Val Asp Ser Gln Pro Gln Ser Lys Ser Lys Asn Thr Trp	
360 365 370 375	
tac att gat gaa gtt gca gaa gac cct gca aaa tct ctt aca gag ata	1564
Tyr Ile Asp Glu Val Ala Glu Asp Pro Ala Lys Ser Leu Thr Glu Ile	
380 385 390	
tct aca gac ttt gac cgt tct tca cca cca ctc cag cct cct cct gtg	1612
Ser Thr Asp Phe Asp Arg Ser Ser Pro Pro Leu Gln Pro Pro Pro Val	
395 400 405	
aac tca ctg acc acc gag aac aga ttc cac tct tta cca ttc agt ctc	1660
Asn Ser Leu Thr Thr Glu Asn Arg Phe His Ser Leu Pro Phe Ser Leu	
410 415 420	
acc aag atg ccc aat acc aat gga agt att ggc cac agt cca ctt tct	1708
Thr Lys Met Pro Asn Thr Asn Gly Ser Ile Gly His Ser Pro Leu Ser	
425 430 435	
ctg tca gcc cag tct gta atg gaa gag cta aac act gca ccc gtc caa	1756
Leu Ser Ala Gln Ser Val Met Glu Glu Leu Asn Thr Ala Pro Val Gln	
440 445 450 455	
gag agt cca ccc ttg gcc atg cct cct ggg aac tca cat ggt cta gaa	1804
Glu Ser Pro Pro Leu Ala Met Pro Pro Gly Asn Ser His Gly Leu Glu	
460 465 470	
gtg ggc tca ttg gct gaa gtt aag gag aac cct cct ttc tat ggg gta	1852
Val Gly Ser Leu Ala Glu Val Lys Glu Asn Pro Pro Phe Tyr Gly Val	
475 480 485	



atc cgt tgg atc ggt cag cca cca gga ctg aat gaa gtg ctc gct gga Ile Arg Trp Ile Gly Gln Pro Pro Gly Leu Asn Glu Val Leu Ala Gly 490 495 500	1900
ctg gaa ctg gaa gat gag tgt gca ggc tgt acg gat gga acc ttc aga Leu Glu Leu Glu Asp Glu Cys Ala Gly Cys Thr Asp Gly Thr Phe Arg 505 510 515	1948
ggc act cgg tat ttc acc tgt gcc ctg aag aag gcg ctg ttt gtg aaa Gly Thr Arg Tyr Phe Thr Cys Ala Leu Lys Lys Ala Leu Phe Val Lys 520 525 530 535	1996
ctg aag agc tgc agg cct gac tct agg ttt gca tca ttg cag ccg gtt Leu Lys Ser Cys Arg Pro Asp Ser Arg Phe Ala Ser Leu Gln Pro Val 540 545 550	2044
tcc aat cag att gag cgc tgt aac tct tta gca ttt gga ggc tac tta Ser Asn Gln Ile Glu Arg Cys Asn Ser Leu Ala Phe Gly Gly Tyr Leu 555 560 565	2092
agt gaa gta gta gaa gaa aat act cca cca aaa atg gaa aaa gaa ggc Ser Glu Val Val Glu Glu Asn Thr Pro Pro Lys Met Glu Lys Glu Gly 570 575 580	2140
ttg gag ata atg att ggg aag aag aaa ggc atc cag ggt cat tac aat Leu Glu Ile Met Ile Gly Lys Lys Lys Gly Ile Gln Gly His Tyr Asn 585 590 595	2188
tct tgt tac tta gac tca acc tta ttc tgc tta ttt gct ttt agt tct Ser Cys Tyr Leu Asp Ser Thr Leu Phe Cys Leu Phe Ala Phe Ser Ser 600 605 610 615	2236
gtt ctg gac act gtg tta ctt aga ccc aaa gaa aag aac gat gta gaa Val Leu Asp Thr Val Leu Leu Arg Pro Lys Glu Lys Asn Asp Val Glu 620 625 630	2284
tat tat agt gaa acc caa gag cta ctg agg aca gaa att gtt aat cct Tyr Tyr Ser Glu Thr Gln Glu Leu Leu Arg Thr Glu Ile Val Asn Pro 635 640 645	2332
ctg aga ata tat gga tat gtg tgt gcc aca aaa att atg aaa ctg agg Leu Arg Ile Tyr Gly Tyr Val Cys Ala Thr Lys Ile Met Lys Leu Arg 650 655 660	2380
aaa ata ctt gaa aag gtg gag gct gca tca gga ttt acc tct gaa gaa Lys Ile Leu Glu Lys Val Glu Ala Ala Ser Gly Phe Thr Ser Glu Glu 665 670 675	2428
aaa gat cct gag gaa ttc ttg aat att ctg ttt cat cat att tta agg Lys Asp Pro Glu Glu Phe Leu Asn Ile Leu Phe His His Ile Leu Arg 680 685 690 695	2476
gta gaa cct ttg cta aaa ata aga tca gca ggt caa aag gta caa gat Val Glu Pro Leu Leu Lys Ile Arg Ser Ala Gly Gln Lys Val Gln Asp 700 705 710	2524
tgt tac ttc tat caa att ttt atg gaa aaa aat gag aaa gtt ggc gtt Cys Tyr Phe Tyr Gln Ile Phe Met Glu Lys Asn Glu Lys Val Gly Val 715 720 725	2572

ccc aca att cag cag ttg tta gaa tgg tct ttt atc aac agt aac ctg Pro Thr Ile Gln Gln Leu Leu Glu Trp Ser Phe Ile Asn Ser Asn Leu 730 735 740	2620
aaa ttt gca gag gca cca tca tgt ctg att att cag atg cct cga ttt Lys Phe Ala Glu Ala Pro Ser Cys Leu Ile Ile Gln Met Pro Arg Phe 745 750 755	2668
gga aaa gac ttt aaa cta ttt aaa aaa att ttt cct tct ctg gaa tta Gly Lys Asp Phe Lys Leu Phe Lys Lys Ile Phe Pro Ser Leu Glu Leu 760 765 770 775	2716
aat ata aca gat tta ctt gaa gac act ccc aga cag tgc cgg ata tgt Asn Ile Thr Asp Leu Leu Glu Asp Thr Pro Arg Gln Cys Arg Ile Cys 780 785 790	2764
gga ggg ctt gca atg tat gag tgt aga gaa tgc tac gac gat ccg gac Gly Gly Leu Ala Met Tyr Glu Cys Arg Glu Cys Tyr Asp Asp Pro Asp 795 800 805	2812
atc tca gct gga aaa atc aag cag ttt tgt aaa acc tgc aac act caa Ile Ser Ala Gly Lys Ile Lys Gln Phe Cys Lys Thr Cys Asn Thr Gln 810 815 820	2860
gtc cac ctt cat ccg aag agg ctg aat cat aaa tat aac cca gtg tca Val His Leu His Pro Lys Arg Leu Asn His Lys Tyr Asn Pro Val Ser 825 830 835	2908
ctt ccc aaa gac tta ccc gac tgg gac tgg aga cac ggc tgc atc cct Leu Pro Lys Asp Leu Pro Asp Trp Asp Trp Arg His Gly Cys Ile Pro 840 845 850 855	2956
tgc cag aat atg gag tta ttt gct gtt ctc tgc ata gaa aca agc cac Cys Gln Asn Met Glu Leu Phe Ala Val Leu Cys Ile Glu Thr Ser His 860 865 870	3004
tat gtt gct ttt gtg aag tat ggg aag gac gat tct gcc tgg ctc ttc Tyr Val Ala Phe Val Lys Tyr Gly Lys Asp Asp Ser Ala Trp Leu Phe 875 880 885	3052
ttt gac agc atg gcc gat cgg gat ggt ggt cag aat ggc ttc aac att Phe Asp Ser Met Ala Asp Arg Asp Gly Gly Gln Asn Gly Phe Asn Ile 890 895 900	3100
cct caa gtc acc cca tgc cca gaa gta gga gag tac ttg aag atg tct Pro Gln Val Thr Pro Cys Pro Glu Val Gly Glu Tyr Leu Lys Met Ser 905 910 915	3148
ctg gaa gac ctg cat tcc ttg gac tcc agg aga atc caa ggc tgt gca Leu Glu Asp Leu His Ser Leu Asp Ser Arg Arg Ile Gln Gly Cys Ala 920 925 930 935	3196
cga aga ctg ctt tgt gat gca tat atg tgc atg tac cag agt cca aca Arg Arg Leu Leu Cys Asp Ala Tyr Met Cys Met Tyr Gln Ser Pro Thr 940 945 950	3244
atg agt ttg tac aaa taa ctggggtcat cgggaaaggc aaagaaactg Met Ser Leu Tyr Lys 955	3292
aaggcagagt cctaacgttg catcttattc gagctggcag ttctgttcac gtccattgcc	3352



tatgtagcat ttacatttat taggtattat aagtaatcta gagattattt aattaaaata 5212  
 tacaggagga tgtgtgttta tatgccagaa attctgtacc attttgtatc aggggaattga 5272  
 gcattcttcag atgttggtat ctgcagggat cctggaacca aacctctgca gatactaagg 5332  
 gctgacgatac taggtaagac tggatttaac agttggaaa 5371

<210> 4  
 <211> 956  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Met Ser Ser Gly Leu Trp Ser Gln Glu Lys Val Thr Ser Pro Tyr Trp  
 1 5 10 15

Glu Glu Arg Ile Phe Tyr Leu Leu Leu Gln Glu Cys Ser Val Thr Asp  
 20 25 30

Lys Gln Thr Gln Lys Leu Leu Lys Val Pro Lys Gly Ser Ile Gly Gln  
 35 40 45

Tyr Ile Gln Asp Arg Ser Val Gly His Ser Arg Ile Pro Ser Ala Lys  
 50 55 60

Gly Lys Lys Asn Gln Ile Gly Leu Lys Ile Leu Glu Gln Pro His Ala  
 65 70 75 80

Val Leu Phe Val Asp Glu Lys Asp Val Val Glu Ile Asn Glu Lys Phe  
 85 90 95

Thr Glu Leu Leu Leu Ala Ile Thr Asn Cys Glu Glu Arg Phe Ser Leu  
 100 105 110

Phe Lys Asn Arg Asn Arg Leu Ser Lys Gly Leu Gln Ile Asp Val Gly  
 115 120 125

Cys Pro Val Lys Val Gln Leu Arg Ser Gly Glu Glu Lys Phe Pro Gly  
 130 135 140

Val Val Arg Phe Arg Gly Pro Leu Leu Ala Glu Arg Thr Val Ser Gly  
 145 150 155 160

Ile Phe Phe Gly Val Glu Leu Leu Glu Glu Gly Arg Gly Gln Gly Phe  
 165 170 175

Thr Asp Gly Val Tyr Gln Gly Lys Gln Leu Phe Gln Cys Asp Glu Asp  
180 185 190

Cys Gly Val Phe Val Ala Leu Asp Lys Leu Glu Leu Ile Glu Asp Asp  
195 200 205

Asp Thr Ala Leu Glu Ser Asp Tyr Ala Gly Pro Gly Asp Thr Met Gln  
210 215 220

Val Glu Leu Pro Pro Leu Glu Ile Asn Ser Arg Val Ser Leu Lys Val  
225 230 235 240

Gly Glu Thr Ile Glu Ser Gly Thr Val Ile Phe Cys Asp Val Leu Pro  
245 250 255

Gly Lys Glu Ser Leu Gly Tyr Phe Val Gly Val Asp Met Asp Asn Pro  
260 265 270

Ile Gly Asn Trp Asp Gly Arg Phe Asp Gly Val Gln Leu Cys Ser Phe  
275 280 285

Ala Cys Val Glu Ser Thr Ile Leu Leu His Ile Asn Asp Ile Ile Pro  
290 295 300

Ala Leu Ser Glu Ser Val Thr Gln Glu Arg Arg Pro Pro Lys Leu Ala  
305 310 315 320

Phe Met Ser Arg Gly Val Gly Asp Lys Gly Ser Ser Ser His Asn Lys  
325 330 335

Pro Lys Ala Thr Gly Ser Thr Ser Asp Pro Gly Asn Arg Asn Arg Ser  
340 345 350

Glu Leu Phe Tyr Thr Leu Asn Gly Ser Ser Val Asp Ser Gln Pro Gln  
355 360 365

Ser Lys Ser Lys Asn Thr Trp Tyr Ile Asp Glu Val Ala Glu Asp Pro  
370 375 380

Ala Lys Ser Leu Thr Glu Ile Ser Thr Asp Phe Asp Arg Ser Ser Pro  
385 390 395 400

Pro Leu Gln Pro Pro Pro Val Asn Ser Leu Thr Thr Glu Asn Arg Phe  
405 410 415

His Ser Leu Pro Phe Ser Leu Thr Lys Met Pro Asn Thr Asn Gly Ser  
420 425 430

Ile Gly His Ser Pro Leu Ser Leu Ser Ala Gln Ser Val Met Glu Glu  
435 440 445

Leu Asn Thr Ala Pro Val Gln Glu Ser Pro Pro Leu Ala Met Pro Pro  
450 455 460

Gly Asn Ser His Gly Leu Glu Val Gly Ser Leu Ala Glu Val Lys Glu  
465 470 475 480

Asn Pro Pro Phe Tyr Gly Val Ile Arg Trp Ile Gly Gln Pro Pro Gly  
485 490 495

Leu Asn Glu Val Leu Ala Gly Leu Glu Leu Glu Asp Glu Cys Ala Gly  
500 505 510

Cys Thr Asp Gly Thr Phe Arg Gly Thr Arg Tyr Phe Thr Cys Ala Leu  
515 520 525

Lys Lys Ala Leu Phe Val Lys Leu Lys Ser Cys Arg Pro Asp Ser Arg  
530 535 540

Phe Ala Ser Leu Gln Pro Val Ser Asn Gln Ile Glu Arg Cys Asn Ser  
545 550 555 560

Leu Ala Phe Gly Gly Tyr Leu Ser Glu Val Val Glu Glu Asn Thr Pro  
565 570 575

Pro Lys Met Glu Lys Glu Gly Leu Glu Ile Met Ile Gly Lys Lys Lys  
580 585 590

Gly Ile Gln Gly His Tyr Asn Ser Cys Tyr Leu Asp Ser Thr Leu Phe  
595 600 605

Cys Leu Phe Ala Phe Ser Ser Val Leu Asp Thr Val Leu Leu Arg Pro  
610 615 620

Lys Glu Lys Asn Asp Val Glu Tyr Tyr Ser Glu Thr Gln Glu Leu Leu  
625 630 635 640

Arg Thr Glu Ile Val Asn Pro Leu Arg Ile Tyr Gly Tyr Val Cys Ala  
645 650 655

Thr Lys Ile Met Lys Leu Arg Lys Ile Leu Glu Lys Val Glu Ala Ala  
660 665 670

Ser Gly Phe Thr Ser Glu Glu Lys Asp Pro Glu Glu Phe Leu Asn Ile  
675 680 685

Leu Phe His His Ile Leu Arg Val Glu Pro Leu Leu Lys Ile Arg Ser  
690 695 700

Ala Gly Gln Lys Val Gln Asp Cys Tyr Phe Tyr Gln Ile Phe Met Glu  
705 710 715 720

Lys Asn Glu Lys Val Gly Val Pro Thr Ile Gln Gln Leu Leu Glu Trp  
725 730 735

Ser Phe Ile Asn Ser Asn Leu Lys Phe Ala Glu Ala Pro Ser Cys Leu  
740 745 750

Ile Ile Gln Met Pro Arg Phe Gly Lys Asp Phe Lys Leu Phe Lys Lys  
755 760 765

Ile Phe Pro Ser Leu Glu Leu Asn Ile Thr Asp Leu Leu Glu Asp Thr  
770 775 780

Pro Arg Gln Cys Arg Ile Cys Gly Gly Leu Ala Met Tyr Glu Cys Arg  
785 790 795 800

Glu Cys Tyr Asp Asp Pro Asp Ile Ser Ala Gly Lys Ile Lys Gln Phe  
805 810 815

Cys Lys Thr Cys Asn Thr Gln Val His Leu His Pro Lys Arg Leu Asn  
820 825 830

His Lys Tyr Asn Pro Val Ser Leu Pro Lys Asp Leu Pro Asp Trp Asp  
835 840 845

Trp Arg His Gly Cys Ile Pro Cys Gln Asn Met Glu Leu Phe Ala Val  
850 855 860

Leu Cys Ile Glu Thr Ser His Tyr Val Ala Phe Val Lys Tyr Gly Lys  
865 870 875 880

Asp Asp Ser Ala Trp Leu Phe Phe Asp Ser Met Ala Asp Arg Asp Gly  
885 890 895

Gly Gln Asn Gly Phe Asn Ile Pro Gln Val Thr Pro Cys Pro Glu Val  
900 905 910

Gly Glu Tyr Leu Lys Met Ser Leu Glu Asp Leu His Ser Leu Asp Ser  
915 920 925

Arg Arg Ile Gln Gly Cys Ala Arg Arg Leu Leu Cys Asp Ala Tyr Met  
930 935 940

Cys Met Tyr Gln Ser Pro Thr Met Ser Leu Tyr Lys  
945 950 955